

## **RAW SEQUENCE LISTING**

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Application Serial Number: 10/006,305A  
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PATENT APPLICATION: US/10/006,305A

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3 <110> APPLICANT: PRUSSAK, CHARLES E.
4      KIPPS, THOMAS J.
5      CANTWELL, MARK J.
7 <120> TITLE OF INVENTION: NOVEL CHIMERIC TNF LIGANDS
9 <130> FILE REFERENCE: 041673-2092
11 <140> CURRENT APPLICATION NUMBER: 10/006,305A
12 <141> CURRENT FILING DATE: 2001-12-06
14 <160> NUMBER OF SEQ ID NOS: 8
16 <170> SOFTWARE: PatentIn Ver. 3.2
18 <210> SEQ ID NO: 1
19 <211> LENGTH: 771
20 <212> TYPE: DNA
21 <213> ORGANISM: Artificial Sequence
23 <220> FEATURE:
24 <223> OTHER INFORMATION: Description of Artificial Sequence: Chimeric DNA construct
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26      III of hCD154
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30 atgaaaattt ttatgtattt acttactgtt ttttttatca cccagatgtat tgggtcagca 120
31 ctttttgcgt tgtagtcttca tagaaggctg gacaagatag aagatgaaag gaatcttcatt 180
32 gaagattttt tattcatgaa aacgatacag agatgcaaca caggagaaag atccttattcc 240
33 ttactgaact gtgaggagat taaaagccag tttgaaggct ttgtgaagga tataatgtta 300
34 aacaaagagg agacgaaagaa agatgaggat cctgttagccc atgttgtagc aaaccctcaa 360
35 gctgaggggc agctccagtg gctgaaccgc cgggccaatg ccctcctggc caatggcgtg 420
36 gagctgagag ataaccagct ggtggtgcca tcagagggcc ttgtacctcat ctactcccg 480
37 gtcctcttca agggccaagg ctgcccctcc acccatgtgc tcctcaccca caccatcagc 540
38 cgcacatcgccg tctccttacca gaccaaggc aacccctctt ctgccccatc gagccctgc 600
39 cagagggaga ccccagaggg ggctgaggcc aagccctggat atgagcccat ctatctggaa 660
40 ggggtcttcc agctggagaa gggtgaccga ctcaagcgtg agatcaatcg gcccactat 720
41 ctcgactttg cggagtctgg gcaggtctac tttgaatca ttgtctgtg a 771
44 <210> SEQ ID NO: 2
45 <211> LENGTH: 580
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47 <213> ORGANISM: Artificial Sequence
49 <220> FEATURE:
50 <223> OTHER INFORMATION: Description of Artificial Sequence: Chimeric DNA construct
51      comprising Domain IV of hTNFa linked to Domains I, II, and
52      III of hCD70
54 <400> SEQUENCE: 2
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56 gctgcttgg tcccatggt cgccggcttg gtgatctgcc tcgtgggtgtg catccagcgc 120
57 ttgcacagg ctgcggatcc tgtagcccat gttgttagcaa accctcaagc tgagggcag 180

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58 ctccagtggc tgaaccgccc gcccaatgcc ctcctggcca atggcggtt gctgagagat 240  
 59 aaccagctgg tggtgccatc agagggcctg tacctcatct actcccagg cctcttaaag 300  
 60 ggccaaaggct gccccccac ccatgtgctc ctcacccaca ccatcagccg catgcggcgtc 360  
 61 tcctaccaga ccaaggtaa cctccctctt gccatcaaga gccccgtcca gagggagacc 420  
 62 ccagaggggg ctgagccaa gccctggtat gagccatct atctgggagg ggtttccag 480  
 63 ctggagaagg gtgaccgact cagcgcttag atcaatcgcc ccgactatct cgactttgcg 540  
 64 gagtctggc aggtctactt tggaaatcatc gctctgtgaa 580  
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 68 <211> LENGTH: 837  
 69 <212> TYPE: DNA  
 70 <213> ORGANISM: Artificial Sequence  
 72 <220> FEATURE:  
 73 <223> OTHER INFORMATION: Description of Artificial Sequence: Chimeric DNA construct  
 74 comprising Domain IV of hTNFa linked to Domains I, II, III  
 75 of hFasL  
 77 <400> SEQUENCE: 3  
 78 atgcagcgc cttcaatta cccatatccc cagatctact gggtggacag cagtgccagc 60  
 79 tctccctggg cccctccagg cacagttctt ccctgtccaa cctctgtgcc cagaaggcct 120  
 80 ggtcaaaggaa ggccaccacc accacccgca cggccaccac taccacctcc gcccggccg 180  
 81 ccaccactgc ctccactacc gtcgcaccc ctgaagaaga gagggaaacca cagcacaggc 240  
 82 ctgtgtctcc ttgtatgtt tttcatgtt ctgggtgcct tggttaggatt gggcctgggg 300  
 83 atgttcagc tcttccaccc acagaaggag ctggcagaac tccgagatgc taccagccag 360  
 84 atgcacacag catcatctt ggagaagcaa gcggatcctg tagcccatgt tgtagcaaac 420  
 85 cctcaagctg agggcagct ccagtggctg aaccggccgg ccaatgcctt cctggccaaat 480  
 86 ggcgtggagc tgagagataa ccagctggcgt gtgcacatcag agggcctgtt cctcatctac 540  
 87 tcccagggtcc tcttcaaggg ccaaggctgc ccctccaccc atgtgtctt caccacacc 600  
 88 atcagccgca tcggcgctc ctaccagacc aaggtcaacc tccctcttgc catcaagago 660  
 89 ccctggcaga gggagacccc agagggggct gaggccaagc cctggatgaa gcccatttat 720  
 90 ctgggagggg tcttccagct ggagaagggtt gaccgactca qcgcgtgagat caatcgcccc 780  
 91 gactatctcg actttgcgga gtctggcag gtctactttt gaatcattgc tctgtga 837  
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 95 <212> TYPE: DNA  
 96 <213> ORGANISM: Artificial Sequence  
 98 <220> FEATURE:  
 99 <223> OTHER INFORMATION: Description of Artificial Sequence: Chimeric DNA construct  
 100 comprising Domain IV of hTNFa linked to Domains I, II, and  
 101 III of hTRAIL  
 103 <400> SEQUENCE: 4  
 104 atggctatga tggagggtcca ggggggaccc agcctggac agacctgcgt gctgatcg 60  
 105 atcttcacag tgctctgtca gtctctctgt gtggctgtt cttacgtgtt ctttaccaac 120  
 106 gagctgaagc agatgcagga caagtactcc aaaagtggca ttgcttgcctt cttaaaaagaa 180  
 107 gatgacagtt attgggaccc caatgacgaa gaggtatga acagccccgt ctggcaagtc 240  
 108 aagtggcaac tccgtcagct cggttagaaag atgatgttga gaacctctga gggaaaccatt 300  
 109 tctacagttc aagaaaagca acaaaaatatt tctcccttag tgagagaaaag aggtcctcag 360  
 110 agagtagcgg atcctgttagc ccatgttgc gcaaaccctc aagctgaggg gcagctccag 420  
 111 tggctgaacc gcccggccaa tgccctctt gccaatggcg tggagctgag agataaccag 480  
 112 ctgggtgtgc catcagaggg cctgtaccc atctactccc aggttctt caagggccaa 540  
 113 ggctgccccctt ccacccatgt gtcctcacc cacaccatca gccgcacgc cgtctctac 600

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 Output Set: N:\CRF4\10292004\J006305A.raw

114 cagaccaagg tcaacctcct ctctgccatc aagagccctt gccagagggaa gaccccagag 660  
 115 ggggctgagg ccaagccctg gtatgagccc atctatctgg gaggggtctt ccagctggag 720  
 116 aagggtgacc gactcagcgc tgagatcaat cggcccgact atctcgactt tgccggagtct 780  
 117 gggcaggtct actttggaat cattgctctg tga 813  
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 121 <211> LENGTH: 256  
 122 <212> TYPE: PRT  
 123 <213> ORGANISM: Artificial Sequence  
 125 <220> FEATURE:  
 126 <223> OTHER INFORMATION: Description of Artificial Sequence: Chimeric TNFa  
 127 polypeptide encoded by the DNA sequence of SEQ ID NO:1  
 129 <400> SEQUENCE: 5  
 130 Met Ile Glu Thr Tyr Asn Gln Thr Ser Pro Arg Ser Ala Ala Thr Gly  
 131 1 5 10 15  
 133 Leu Pro Ile Ser Met Lys Ile Phe Met Tyr Leu Leu Thr Val Phe Leu  
 134 20 25 30  
 136 Ile Thr Gln Met Ile Gly Ser Ala Leu Phe Ala Val Tyr Leu His Arg  
 137 35 40 45  
 139 Arg Leu Asp Lys Ile Glu Asp Glu Arg Asn Leu His Glu Asp Phe Val  
 140 50 55 60  
 142 Phe Met Lys Thr Ile Gln Arg Cys Asn Thr Gly Glu Arg Ser Leu Ser  
 143 65 70 75 80  
 145 Leu Leu Asn Cys Glu Glu Ile Lys Ser Gln Phe Glu Gly Phe Val Lys  
 146 85 90 95  
 148 Asp Ile Met Leu Asn Lys Glu Glu Thr Lys Lys Asp Glu Asp Pro Val  
 149 100 105 110  
 151 Ala His Val Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu  
 152 115 120 125  
 154 Asn Arg Arg Ala Asn Ala Leu Ala Asn Gly Val Glu Leu Arg Asp  
 155 130 135 140  
 157 Asn Gln Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln  
 158 145 150 155 160  
 160 Val Leu Phe Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr  
 161 165 170 175  
 163 His Thr Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu  
 164 180 185 190  
 166 Leu Ser Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala  
 167 195 200 205  
 169 Glu Ala Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln  
 170 210 215 220  
 172 Leu Glu Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr  
 173 225 230 235 240  
 175 Leu Asp Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu  
 176 245 250 255  
 182 <210> SEQ ID NO: 6  
 183 <211> LENGTH: 192  
 184 <212> TYPE: PRT  
 185 <213> ORGANISM: Artificial Sequence  
 187 <220> FEATURE:

RAW SEQUENCE LISTING  
 PATENT APPLICATION: US/10/006,305A DATE: 10/29/2004  
 TIME: 13:08:30

Input Set : A:\41673292.app  
 Output Set: N:\CRF4\10292004\J006305A.raw

188 <223> OTHER INFORMATION: Description of Artificial Sequence: Chimeric TBFa  
 189 polypeptide encoded by the DNA sequence of SEQ ID NO:2  
 191 <400> SEQUENCE: 6  
 192 Met Pro Glu Glu Gly Ser Gly Cys Ser Val Arg Arg Arg Pro Tyr Gly  
 193 1 5 10 15  
 195 Cys Val Leu Arg Ala Ala Leu Val Pro Leu Val Ala Gly Leu Val Ile  
 196 20 25 30  
 198 Cys Leu Val Val Cys Ile Gln Arg Phe Ala Gln Ala Ala Asp Pro Val  
 199 35 40 45  
 201 Ala His Val Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu  
 202 50 55 60  
 204 Asn Arg Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp  
 205 65 70 75 80  
 207 Asn Gln Leu Val Val Pro Ser Glu Gly Leu Tyr Leu Ile Tyr Ser Gln  
 208 85 90 95  
 210 Val Leu Phe Lys Gly Gln Gly Cys Pro Ser Thr His Val Leu Leu Thr  
 211 100 105 110  
 213 His Thr Ile Ser Arg Ile Ala Val Ser Tyr Gln Thr Lys Val Asn Leu  
 214 115 120 125  
 216 Leu Ser Ala Ile Lys Ser Pro Cys Gln Arg Glu Thr Pro Glu Gly Ala  
 217 130 135 140  
 219 Glu Ala Lys Pro Trp Tyr Glu Pro Ile Tyr Leu Gly Gly Val Phe Gln  
 220 145 150 155 160  
 222 Leu Glu Lys Gly Asp Arg Leu Ser Ala Glu Ile Asn Arg Pro Asp Tyr  
 223 165 170 175  
 225 Leu Asp Phe Ala Glu Ser Gly Gln Val Tyr Phe Gly Ile Ile Ala Leu  
 226 180 185 190  
 232 <210> SEQ ID NO: 7  
 233 <211> LENGTH: 278  
 234 <212> TYPE: PRT  
 235 <213> ORGANISM: Artificial Sequence  
 237 <220> FEATURE:  
 238 <223> OTHER INFORMATION: Description of Artificial Sequence: Chimeric TNFa  
 239 polypeptide encoded by the DNA sequence of SEQ ID NO:3  
 241 <400> SEQUENCE: 7  
 242 Met Gln Gln Pro Phe Asn Tyr Pro Tyr Pro Gln Ile Tyr Trp Val Asp  
 243 1 5 10 15  
 245 Ser Ser Ala Ser Ser Pro Trp Ala Pro Pro Gly Thr Val Leu Pro Cys  
 246 20 25 30  
 248 Pro Thr Ser Val Pro Arg Arg Pro Gly Gln Arg Arg Pro Pro Pro Pro  
 249 35 40 45  
 251 Pro Pro Pro Pro Leu Pro Pro Pro Pro Pro Pro Pro Pro Leu Pro  
 252 50 55 60  
 254 Pro Leu Pro Leu Pro Pro Leu Lys Lys Arg Gly Asn His Ser Thr Gly  
 255 65 70 75 80  
 257 Leu Cys Leu Leu Val Met Phe Phe Met Val Leu Val Ala Leu Val Gly  
 258 85 90 95  
 260 Leu Gly Leu Gly Met Phe Gln Leu Phe His Leu Gln Lys Glu Leu Ala  
 261 100 105 110

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 Output Set: N:\CRF4\10292004\J006305A.raw

263 Glu Leu Arg Glu Ser Thr Ser Gln Met His Thr Ala Ser Ser Leu Glu  
 264 115 120 125  
 266 Lys Gln Ala Asp Pro Val Ala His Val Val Ala Asn Pro Gln Ala Glu  
 267 130 135 140  
 269 Gly Gln Leu Gln Trp Leu Asn Arg Arg Ala Asn Ala Leu Leu Ala Asn  
 270 145 150 155 160  
 272 Gly Val Glu Leu Arg Asp Asn Glu Leu Val Val Pro Ser Glu Gly Leu  
 273 165 170 175  
 275 Tyr Leu Ile Tyr Ser Gln Val Leu Phe Lys Gly Gln Gly Cys Pro Ser  
 276 180 185 190  
 278 Thr His Val Leu Leu Thr His Thr Ile Ser Arg Ile Ala Val Ser Tyr  
 279 195 200 205  
 281 Gln Thr Lys Val Asn Leu Leu Ser Ala Ile Lys Ser Pro Cys Gln Arg  
 282 210 215 220  
 284 Glu Thr Pro Glu Gly Ala Glu Ala Lys Pro Trp Tyr Glu Pro Ile Tyr  
 285 225 230 235 240  
 287 Leu Gly Gly Val Phe Gln Leu Glu Lys Gly Asp Arg Leu Ser Ala Glu  
 288 245 250 255  
 290 Ile Asn Arg Pro Asp Tyr Leu Asp Phe Ala Glu Ser Gly Gln Val Tyr  
 291 260 265 270  
 293 Phe Gly Ile Ile Ala Leu  
 294 275  
 297 <210> SEQ ID NO: 8  
 298 <211> LENGTH: 270  
 299 <212> TYPE: PRT  
 300 <213> ORGANISM: Artificial Sequence  
 302 <220> FEATURE:  
 303 <223> OTHER INFORMATION: Description of Artificial Sequence: Chimeric TNFa  
 304 polypeptide encoded by the DNA sequence of SEQ ID NO:4  
 306 <400> SEQUENCE: 8  
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 308 1 5 10 15  
 310 Val Leu Ile Val Ile Phe Thr Val Leu Leu Gln Ser Leu Cys Val Ala  
 311 20 25 30  
 313 Val Thr Tyr Val Tyr Phe Thr Asn Glu Leu Lys Gln Met Gln Asp Lys  
 314 35 40 45  
 316 Tyr Ser Lys Ser Gly Ile Ala Cys Phe Leu Lys Glu Asp Asp Ser Tyr  
 317 50 55 60  
 319 Trp Asp Pro Asn Asp Glu Glu Ser Met Asn Ser Pro Cys Trp Gln Val  
 320 65 70 75 80  
 322 Lys Trp Gln Leu Arg Gln Leu Val Arg Lys Met Ile Leu Arg Thr Ser  
 323 85 90 95  
 325 Glu Glu Thr Ile Ser Thr Val Gln Glu Lys Gln Gln Asn Ile Ser Pro  
 326 100 105 110  
 328 Leu Val Arg Glu Arg Glu Pro Gln Arg Val Ala Asp Pro Val Ala His  
 329 115 120 125  
 331 Val Val Ala Asn Pro Gln Ala Glu Gly Gln Leu Gln Trp Leu Asn Arg  
 332 130 135 140  
 334 Arg Ala Asn Ala Leu Leu Ala Asn Gly Val Glu Leu Arg Asp Asn Gln

**VERIFICATION SUMMARY**

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DATE: 10/29/2004

TIME: 13:08:31

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